

2651224\_1.TXT  
SEQUENCE LISTINGS

<110> INJE UNIVERSITY  
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<140> US 10/578,839  
<141> 2006-05-10  
<150> KR 10-2003-0079897  
<151> 2003-11-12  
<150> PCT/KR2004/000545  
<151> 2004-03-15  
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<213> Artificial Sequence

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gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180

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tcccaaactg gagacgttgt ctgggataca aaggcagtcc agcccccttg gacttggtgg 240  
cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg 300  
ggaaccgatg tctcgccctc taaacgagtc agacctccgg actcagacta tactgccgt 360  
tataagcaaa tcacctgggg agccataggg tgtagctacc ctcggctag gactagaatg 420  
gcaagctcta ctttctacgt atgtccccgg gatggccgga cccttcaga agctagaagg 480  
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<223> heavy chain (H) variable region

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<222> (391)..(738)  
<223> Light chain (L) variable region

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<222> (739)..(777)  
<223> Pres1 Tag

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<222> (778)..(786)  
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cctggacaac gccttgagtg gatggatataat ttttctcctg gcaacgatga ttttaataac 180  
tcccagaagt tccagggacg cgtacaatc actgcagaca aatccgcgag cacagcctac 240  
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gttttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaaggtg 720  
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<212> PRT  
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<210> 10  
<211> 2871  
<212> DNA  
<213> Artificial Sequence

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<223> ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

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<210> 11  
<211> 956  
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<223> ScFv-GaLV Env GP chimeric ligand (FvGEL199)

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Leu Ser Cys Val Phe Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn  
35 40 45  
Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly  
50 55 60  
Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp  
65 70 75 80  
Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser  
85 90 95  
Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro  
100 105 110  
Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala  
115 120 125  
Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr  
130 135 140  
Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg  
145 150 155 160  
Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr  
165 170 175  
Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr  
180 185 190  
Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Ser Gln Val Gln Leu  
195 200 205  
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val  
210 215 220  
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp  
225 230 235 240  
Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser  
245 250 255  
Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val  
260 265 270

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Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser  
275 280 285  
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu  
290 295 300  
Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly  
305 310 315 320  
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Asp Ile  
325 330 335  
Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg  
340 345 350  
Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn  
355 360 365  
Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
370 375 380  
Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp  
385 390 395 400  
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
405 410 415  
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr  
420 425 430  
Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala  
435 440 445  
Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala  
450 455 460  
Ala Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His  
465 470 475 480  
Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly  
485 490 495  
Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe  
500 505 510  
Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile  
515 520 525  
Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu  
530 535 540  
Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Pro Leu Pro Pro  
545 550 555 560  
Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu  
565 570 575  
Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu  
580 585 590  
Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln  
595 600 605

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Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser  
 610 615 620  
 Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala  
 625 630 635 640  
 Ser Ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp  
 645 650 655  
 Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu  
 660 665 670  
 Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr  
 675 680 685  
 Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn  
 690 695 700  
 His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr  
 705 710 715 720  
 Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile  
 725 730 735  
 Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp  
 740 745 750  
 Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala  
 755 760 765  
 Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr  
 770 775 780  
 Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu  
 785 790 795 800  
 Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser  
 805 810 815  
 Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn  
 820 825 830  
 Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala  
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 Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val  
 850 855 860  
 Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu  
 865 870 875 880  
 Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser  
 885 890 895  
 Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu  
 900 905 910  
 Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val  
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 Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg  
 930 935 940

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Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu  
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